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identified by microarray analysis**

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Candidate genes for the progression of malignant gliomas identified by microarray analysis

Negative results in the logarithmic M AstroIII/GBM quotient represents upregulation of the gene

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It was brought to our attention, that there is a misinterpretation of the data in the text of our article [2]. After comparing our data with the original ones, we found that the microarray data as shown in our *Table 1* [2] are correct. However, in the text the column indicating the direction of expression “down or up” has been mistaken: “down” in this

table refers to a lower expression in anaplastic astrocytomas (AA) relative to glioblastomas (GBM).

This is consistent with the other values given in the Table. The median expression levels for both groups were calculated as mean log₂-ratios. A negative result in the logarithmic M AstroIII/GBM quotient represents an upregulation of the gene in GBM. In this regard the direction of the expression level (FC) in column six can be misleading, but represents correctly the direction from GBM to AA and not vice versa, as we erroneously have used in the discussion [2].

Unfortunately, the real-time PCR results in the same (small) group of tumors did in fact falsely indorse the misinterpreted results. Recent further investigation in a larger group of tumors (34 samples) of the same histology has meanwhile put into perspective the results of IL-13R α 2 and *Olig2*. *Olig2* had an almost 4-fold higher expression in AA (0,1146) compared to GBM (0,0294) with statistical significance ($p=0,025$). IL-13R α 2 showed now a near equal expression (AA 2,5078, GBM 2,7831) with no statistical significance. Previous results [1, 5] showed significant decline of gene expression with tumor grade and lowest expression of *Olig2* in GBM, which is now consistent with our further analysis and correctly interpreted array results. The equal expression of IL-13R α 2 in our recent larger PCR series does not answer satisfactorily the question of expression differences between AA and GBM.

These differences in real-time PCR quantification compared to the array results make their confirmation insecure. In similar studies Hoelzinger et al. confirmed only 19 genes out of 21 by quantitative RT-PCR [3] and van den Boom et al. in 9 out of 12 cases [6]. According to Vandesompele

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et al. normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes might be the solution and could open the possibility of studying the biological relevance of small expression differences [7]. However, small series, such as ours, seem to be at risk for false confirmation and even further studies in larger groups can be misleading. Additional tissue based investigation, such as immunohistochemistry or in situ hybridization may in future be more valuable to support the results from the PCR studies

It will be our obligation for the future, to provide profound data on a large amount of tissue samples and different quantification methods to clarify these uncertainties and initial microarray analysis, especially regarding IL-13R α 2, which plays a critical biologic role in IL-13 cytotoxin-mediated therapy for GBM [4]. Any possible beneficial role of this treatment regimen for GBM rather than for AA needs to be confirmed by a larger series. Accordingly, clinical trials addressing the prognostic relevance may highlight the functional significance. The conclusion of our article regarding the powerful approach of gene expression profiling to identify transcriptional differences of significance in gliomas remains [2], but its confirmation seems challenging and needs expansion to multiple quantification methods in order to avoid interpretation mistakes.

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